

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,619  
Source: PCR  
Date Processed by STIC: 3/3/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/524,619

TIME: 12:54:53

Input Set : A:\DAVI251.001APC\_sequence\_listing.TXT

Output Set: N:\CRF4\03032006\J524619.raw

3 <110> APPLICANT: Melbourne Health  
 4 Jane, Stephen (US Only)  
 5 Wilanowski, Tomasz (US only)  
 6 Ting, Stephen (US only)  
 8 <120> TITLE OF INVENTION: MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS  
 10 <130> FILE REFERENCE: DAVI251.001APC  
 12 <140> CURRENT APPLICATION NUMBER: US 10/524,619  
 13 <141> CURRENT FILING DATE: 2005-02-09  
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01006  
 16 <151> PRIOR FILING DATE: 2003-08-08  
 18 <150> PRIOR APPLICATION NUMBER: US 60/402055  
 19 <151> PRIOR FILING DATE: 2002-08-09  
 21 <150> PRIOR APPLICATION NUMBER: AU2002951579  
 22 <151> PRIOR FILING DATE: 2002-08-22  
 24 <160> NUMBER OF SEQ ID NOS: 46  
 26 <170> SOFTWARE: PatentIn version 3.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 1881  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: human  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: CDS  
 35 <222> LOCATION: (94)..(1323)  
 38 <400> SEQUENCE: 1

39	ataagagagg ccatctgaca gctccagata cgacagtcac tgtctccata gcaacgatgc	60
41	ctaccctcctc catcaagaca gaaacccagc cac atg gct tcg ctg tgg gaa tcc	114
42		
43	Met Ala Ser Leu Trp Glu Ser	
45	ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg	162
46	Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser	
47	10 15 20	
49	atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa	210
50	Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln	
51	25 30 35	
53	atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg	258
54	Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg	
55	40 45 50 55	
57	aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa	306
58	Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys	
59	60 65 70	
61	tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa	354
62	Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys	
63	75 80 85	

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65 ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga      402
66 Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly
67          90          95          100
69 atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt      450
70 Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe
71      105          110          115
73 gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg      498
74 Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp
75 120          125          130          135
77 cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac      546
78 His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp
79          140          145          150
81 tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat      594
82 Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr
83          155          160          165
85 aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc      642
86 Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe
87      170          175          180
89 atc tct gtc aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg      590
90 Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
91      185          190          195
93 aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac      738
94 Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn
95 200          205          210          215
97 cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc      786
98 Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe
99          220          225          230
101 tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa      834
102 Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
103          235          240          245
105 agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac      882
106 Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His
107          250          255          260
109 aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act      930
110 Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr
111          265          270          275
113 cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg      978
114 Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg
115 280          285          290          295
117 ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc      1026
118 Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly
119          300          305          310
121 tct gtc ttg aaa agg ggg ccg tac ggc aca gaa gat gac ttt gct gtc      1074
122 Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val
123          315          320          325
125 cct cct tct acc aag ctg gcc cgg ata gaa gaa cca aag aga gtg ctg      1122
126 Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro Lys Arg Val Leu
127          330          335          340
129 ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc      1170

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130 Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
131      345      350      355
133 aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac      1218
134 Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
135 360      365      370      375
137 gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag      1266
138 Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
139      380      385      390
141 ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat      1314
142 Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
143      395      400      405
145 gag gac acc ttccagctgc agattgaaga agccggggggg tcttacaagc      1363
146 Glu Asp Thr
147      410
149 tcaccctgac ggagatctaa aggcctgcgg gccacagctc cccaggagtt cagtgcaggt      1423
151 gtttctagat cttacggttt ggcaactgca ggtaacccca gtcagccatg tgcgcagcac      1483
153 aggtctatgt cgagggaatg ggttccttgc aggttgagg cggggctgca tctggcttgg      1543
155 tggtagcatt taatctattg cattggtgtt tttcagatga aagagaaatc catataccat      1603
157 tatgtttgaa tttcctgata tatacaggat ttcaagtga aactttattc caagagttaa      1663
159 cagagtctct gggaagcttt aggacatctg ctacgttatt tatcaaaaata ttgggatctc      1723
161 tgccttgatg ctacagtgtc gtgggcctgc tgcctagcag aagtcagaaa aggcgatagg      1783
163 cttggcttta aggatttcgt gcccttgccct gaattcagta caactccact gcctcacggt      1843
165 agcgggagcg cacctgaaga gtacggggggg agccctct      1881
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 410
170 <212> TYPE: PRT
171 <213> ORGANISM: human
173 <400> SEQUENCE: 2
175 Met Ala Ser Leu Trp Glu Ser Pro Gln Gln Cys Ile Ile Leu Ser Pro
176 1      5      10      15
179 Leu Ser Gly Trp Trp Phe Ser Ile Gly Ile Ser Ile Leu Thr Ser Ser
180      20      25      30
183 Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
184      35      40      45
187 Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
188      50      55      60
191 Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
192 65      70      75      80
195 Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
196      85      90      95
199 Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
200      100      105      110
203 Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
204      115      120      125
207 Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
208      130      135      140
211 Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
212 145      150      155      160
215 Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile

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```

216          165          170          175
219 Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
220          180          185          190
223 Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
224          195          200          205
227 Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
228          210          215          220
231 Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
232 225          230          235          240
235 Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
236          245          250          255
239 Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
240          260          265          270
243 Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
244          275          280          285
247 His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
248          290          295          300
251 Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
252 305          310          315          320
255 Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
256          325          330          335
259 Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
260          340          345          350
263 Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
264          355          360          365
267 Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
268          370          375          380
271 Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn
272 385          390          395          400
275 Ile Val Lys His Tyr Ser Asn Glu Asp Thr
276          405          410
279 <210> SEQ ID NO: 3
280 <211> LENGTH: 2361
281 <212> TYPE: DNA
282 <213> ORGANISM: human
284 <220> FEATURE:
285 <221> NAME/KEY: CDS
286 <222> LOCATION: (7)..(1860)
288 <220> FEATURE:
289 <221> NAME/KEY: VARIANT
290 <222> LOCATION: 342
291 <223> OTHER INFORMATION: Xaa = Lys, Ile
294 <400> SEQUENCE: 3
295 agcgcg atg aca cag gag tac gac aac aaa cgg cca gtg ttg gtt ctt      48
296      Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu
297      1          5          10
299 cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat      96
300 Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp
301 15          20          25          30

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303	gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa	144
304	Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys	
305	35 40 45	
307	gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc	192
308	Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly	
309	50 55 60	
311	ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca	240
312	Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr	
313	65 70 75	
315	gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac	288
316	Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn	
317	80 85 90	
319	agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac	336
320	Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn	
321	95 100 105 110	
323	aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat	384
324	Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His	
325	115 120 125	
327	ggc aac cag ctg ggc att gat gag aga ggc cat ctg aca gct tca gat	432
328	Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp	
329	130 135 140	
331	acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag	480
332	Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys	
333	145 150 155	
335	aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg	528
336	Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val	
337	160 165 170	
339	tat cat cct gag ccc act gag cgg gtg gtg gtt ttc gat cgg aay ctc	576
340	Tyr His Pro Glu Pro Thr Glu Arg Val Val Phe Asp Arg Asn Leu	
341	175 180 185 190	
343	aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg	624
344	Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg	
345	195 200 205	
347	cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag	672
348	Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln	
349	210 215 220	
351	gag gtt ttc ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat	720
352	Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn	
353	225 230 235	
355	tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat	768
356	Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr	
357	240 245 250	
359	acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc	816
360	Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr	
361	255 260 265 270	
363	atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag	864
364	Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu	
365	275 280 285	
367	gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt	912

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/03/2006  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 342  
Seq#:4; Xaa Pos. 342  
Seq#:7; Xaa Pos. 117,172  
Seq#:8; Xaa Pos. 117,172  
Seq#:9; N Pos. 2634,2968  
Seq#:11; N Pos. 2973,3307  
Seq#:15; N Pos. 2806

## VERIFICATION SUMMARY

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L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1056  
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:336  
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:439  
L:1133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:583  
L:1290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:112  
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:160  
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2580  
L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2940  
L:1796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2940  
L:1808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3300  
L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2788